

SEQUENCE LISTING

<110> Kinney, Anthony
<120> Hypoallergenic Transgenic Soybeans

<130> BB1432 US NA

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<150> 60/189,823

<151> 16 MARCH 2000

<160> 16

<170> Microsoft Office 97

<210> 1

<211> 1156

<212> DNA

<213> chimeric construct

<400> 1

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<210> 2

<211> 2970

<212> DNA

<213> chimeric construct

<400> 2

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<210> 4
<211> 454
<212> PRT
<213> Glycine max

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          20                      25                      30

Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
          35                      40                      45

Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
          50                      55                      60

Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
          65                      70                      75                      80

Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
          85                      90                      95

Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
          100                      105                      110

Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro
          115                      120                      125

Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
          130                      135                      140

Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
          145                      150                      155                      160

Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
          165                      170                      175

Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
          180                      185                      190

Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
          195                      200                      205

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Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
 210 215 220
 Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
 225 230 235 240
 Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
 245 250 255
 Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
 260 265 270
 Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
 275 280 285
 Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
 290 295 300
 Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
 305 310 315 320
 Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
 325 330 335
 Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
 340 345 350
 Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
 355 360 365
 Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
 370 375 380
 Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
 385 390 395 400
 Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
 405 410 415
 Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
 420 425 430
 Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
 435 440 445
 Val Val Met Asp Val Phe
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<210> 5
 <211> 494
 <212> DNA
 <213> Glycine max

<400> 5
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 actgaggcaa agacttgca gaacctggct gatacataca ggggtccatg cttcaccact 180
 ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcaggac 240
 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300

agatgcatgc agcgctatatt tataaaaaat acaactacta tatactatat ataataagac 360
 tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccgat gtcaagaact 420
 atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataa 480
 agtgctgttg ttgc 494

<210> 6
 <211> 75
 <212> PRT
 <213> Glycine max

<400> 6
 Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu
 1 5 10 15

Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu
 20 25 30

Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys
 35 40 45

Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg
 50 55 60

Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys
 65 70 75

<210> 7
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: P34 gene primer

<400> 7
 gaattcgcgg ccgcatgggt ttccttgtgt 30

<210> 8
 <211> 30
 <212> DNA
 <213> Glycine max

<220>
 <223> Description of Artificial Sequence: P34 gene primer

<400> 8
 gaattcgcgg ccgctcaaag aggagagtga 30

<210> 9
 <211> 701
 <212> DNA
 <213> Glycine max

<400> 9
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 atccacagcc ccaaccttct caggtcaactg ctcttattac acgacctagt tgtccggatc 180
 tgagtatttg cctcaatatt ttaggcgggt ctctaggaac cgtggatgat tgttggtgcc 240
 tcatcggttg tcttggtgac attgaagcca ttgtgtgcct ttgcatccaa ctcagggccc 300
 tcggaatatt aaaccttaac cgtaatttgc agttaatat aaactcctgt ggacgaagct 360

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accggtcaaa cgccacttgc ccccgaaact aagaacagaa tatgtatggc actaattacc 420
atattacttc gtatcatggt gtttggttgt ttgtctgtgt ttaaagttaa ggatgttata 480
cccttcgtgc ctgctacata tatatagtgg gcactataat attaccaata aattaacgtc 540
catatataag aataataata aataaataaa tatttctata caaataaagg ttacgtaatg 600
ttgttggttct cgtggatggg gatcttatct tcctcctcgc tatctttgtt tatcgatttt 660
cagtgaagt tgttcaataa aagtcctttg ttcaacaagt g 701

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<210> 10
 <211> 119
 <212> PRT
 <213> Glycine max

<400> 10
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 20 25 30
 Pro Gln Pro Ser His Val Thr Ala Leu Ile Thr Arg Pro Ser Cys Pro
 35 40 45
 Asp Leu Ser Ile Cys Leu Asn Ile Leu Gly Gly Ser Leu Gly Thr Val
 50 55 60
 Asp Asp Cys Cys Ala Leu Ile Gly Gly Leu Gly Asp Ile Glu Ala Ile
 65 70 75 80
 Val Cys Leu Cys Ile Gln Leu Arg Ala Leu Gly Ile Leu Asn Leu Asn
 85 90 95
 Arg Asn Leu Gln Leu Ile Leu Asn Ser Cys Gly Arg Ser Tyr Pro Ser
 100 105 110
 Asn Ala Thr Cys Pro Arg Thr
 115

<210> 11
 <211> 396
 <212> DNA
 <213> Glycine max

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<400> 11
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cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
gctccaactg gattgtatct cgggtggcacc aaatatatgg tcatccaggg tgaaccgggt 240
gctgtcattc gagggaaagaa gggtcctggt ggtgttactg tgaagaagac cgggtgcggcc 300
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<210> 12
 <211> 131
 <212> PRT
 <213> Glycine max

<400> 12
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Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
 20 25 30

Trp Leu Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
 35 40 45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
 50 55 60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
 65 70 75 80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
 85 90 95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
 100 105 110

Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Asp
 115 120 125

Gln Gly Tyr
 130

<210> 13
 <211> 396
 <212> DNA
 <213> Glycine max

<400> 13
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 cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
 gctccaactg gattgtatct cgggtggcacc aaatatatgg tcatccaggg tgaacccggt 240
 gctgtcattc gagggaagaa gggtcctggt ggtgttactg tgaagaagac cgggtgcggcc 300
 ttgatcattg gcatttatga tgaaccaatg actccaggtc aatgcaacat ggtagttgaa 360
 aggcctggtg attacctcat cgaccagggc tactga 396

<210> 14
 <211> 131
 <212> PRT
 <213> Glycine max

<400> 14
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 1 5 10 15

Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
 20 25 30

Trp Ala Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
 35 40 45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
 50 55 60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
 65 70 75 80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
85 90 95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
100 105 110

Gly Gln Cys Asn Met Val Val Glu Arg Pro Gly Asp Tyr Leu Ile Asp
115 120 125

Gln Gly Tyr
130

<210> 15
<211> 1746
<212> DNA
<213> Glycine max

<400> 15
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<210> 16
<211> 495
<212> PRT
<213> Glycine max

<400> 16
Met Ala Lys Leu Val Phe Ser Leu Cys Phe Leu Leu Phe Ser Gly Cys
1 5 10 15

Cys Phe Ala Phe Ser Ser Arg Glu Gln Pro Gln Gln Asn Glu Cys Gln
20 25 30

Ile	Gln	Lys	Leu	Asn	Ala	Leu	Lys	Pro	Gly	Asn	Arg	Ile	Glu	Ser	Glu	
		35					40					45				
Gly	Gly	Leu	Ile	Glu	Thr	Trp	Asn	Pro	Asn	Asn	Lys	Pro	Phe	Gln	Cys	
	50					55					60					
Ala	Gly	Val	Ala	Leu	Ser	Arg	Cys	Thr	Leu	Asn	Arg	Asn	Ala	Leu	Arg	
65					70					75					80	
Arg	Pro	Ser	Tyr	Thr	Asn	Gly	Pro	Gln	Glu	Ile	Tyr	Ile	Gln	Gln	Gly	
				85					90					95		
Lys	Gly	Ile	Phe	Gly	Met	Ile	Tyr	Pro	Gly	Cys	Ser	Ser	Thr	Phe	Glu	
			100					105					110			
Glu	Pro	Gln	Gln	Pro	Gln	Gln	Arg	Gly	Gln	Ser	Ser	Arg	Pro	Gln	Asp	
		115					120					125				
Arg	His	Gln	Lys	Ile	Tyr	Asn	Ser	Arg	Glu	Gly	Asp	Leu	Ile	Ala	Val	
	130					135					140					
Pro	Thr	Gly	Val	Ala	Trp	Trp	Met	Tyr	Asn	Asn	Glu	Asp	Thr	Pro	Val	
145					150					155					160	
Val	Ala	Val	Ser	Ile	Ile	Asp	Thr	Asn	Ser	Leu	Glu	Asn	Gln	Leu	Asp	
				165					170					175		
Gln	Met	Pro	Arg	Arg	Phe	Tyr	Leu	Ala	Gly	Asn	Gln	Glu	Gln	Glu	Phe	
			180					185					190			
Leu	Lys	Tyr	Gln	Gln	Glu	Gln	Gly	Gly	His	Gln	Ser	Gln	Lys	Gly	Lys	
		195					200					205				
His	Gln	Gln	Glu	Glu	Glu	Asn	Glu	Gly	Gly	Ser	Ile	Leu	Ser	Gly	Phe	
	210					215					220					
Thr	Leu	Glu	Phe	Leu	Glu	His	Ala	Phe	Ser	Val	Asp	Lys	Gln	Ile	Ala	
225					230					235					240	
Lys	Asn	Leu	Gln	Gly	Glu	Asn	Glu	Gly	Glu	Asp	Lys	Gly	Ala	Ile	Val	
			245					250						255		
Thr	Val	Lys	Gly	Gly	Leu	Ser	Val	Ile	Lys	Pro	Pro	Thr	Asp	Glu	Gln	
			260					265					270			
Gln	Gln	Arg	Pro	Gln	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Lys	Pro	
		275					280					285				
Gln	Cys	Lys	Gly	Lys	Asp	Lys	His	Cys	Gln	Arg	Pro	Arg	Gly	Ser	Gln	
	290					295					300					
Ser	Lys	Ser	Arg	Arg	Asn	Gly	Ile	Asp	Glu	Thr	Ile	Cys	Thr	Met	Arg	
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Leu	Arg	His	Asn	Ile	Gly	Gln	Thr	Ser	Ser	Pro	Asp	Ile	Tyr	Asn	Pro	
			325						330					335		
Gln	Ala	Gly	Ser	Val	Thr	Thr	Ala	Thr	Ser	Leu	Asp	Phe	Pro	Ala	Leu	
			340					345					350			

